Fig 1 (1)

```
  1 tacaatgggg tggcggaggt gaagaaacgg ggttacttct atgctagaac gcaaggaaca 19ftf>
      y  n  g  v  a  e  v  k  k  r  g  y  f  y  a  r  t
      y  n  g  v  a  e  v  n  t  e  r  g  a  n  g  q  i

 61 taaaaaaatg tataaaagcg gtaaaaattg ggcagtcgtt acactctcga ctgctgcgct
  1           m  y  k  s  g  k  n  w  a  v  v  t  l  s  t  a  a

121 ggtatttggt gcaacaactg taaatgcatc cgcggacaca aatattgaaa acaatgattc
 18 l  v  f  g  a  t  t  v  n  a  s  a  d  t  n  i  e  n  n  d

181 ttctactgta caagttacaa caggtgataa tgatattgct gttaaaagtg tgacacttgg
 38 s  s  t  v  q  v  t  t  g  d  n  d  i  a  v  k  s  v  t  l

241 tagtggtcaa gttagtgcag ctagtgatac gactattaga acttctgcta atgcaaatag
 58 g  s  g  q  v  s  a  a  s  d  t  t  i  r  t  s  a  n  a  n

301 tgcttcttct gccgctaata cacaaaattc taacagtcaa gtagcaagtt ctgctgcaat
 78 s  a  s  s  a  a  n  t  q  n  s  n  s  q  v  a  s  s  a  a

361 aacatcatct acaagttccg cagcttcatt aaataacaca gatagtaaag cggctcaaga
 98 i  t  s  s  t  s  s  a  a  s  l  n  n  t  d  s  k  a  a  q

421 aaatactaat acagccaaaa atgatgacac gcaaaaagct gcaccagcta acgaatcttc
118 e  n  t  n  t  a  k  n  d  d  t  q  k  a  a  p  a  n  e  s

481 tgaagctaaa aatgaaccag ctgtaaacgt taatgattct tcagctgcaa aaaatgatga
138 s  e  a  k  n  e  p  a  v  n  v  n  d  s  s  a  a  k  n  d

541 tcaacaatcc agtaaaaaga atactaccgc taagttaaac aaggatgctg aaaacgttgt
158 d  q  q  s  s  k  k  n  t  t  a  k  l  n  k  d  a  e  n  v

601 aaaaaaggcg ggaattgatc ctaacagttt aactgatgac cagattaaag cattaaataa
178 v  k  k  a  g  i  d  p  n  s  l  t  d  d  q  i  k  a  l  n
```

Fig 1 (2)

```
661 gatgaacttc tcgaaagctg caaagtctgg tacacaaatg acttataatg atttccaaaa
198 k   m   n   f   s   k   a   a   k   s   g   t   q   m   t   y   n   d   f   q


721 gattgctgat acgttaatca aacaagatgg tcggtacaca gttccattct ttaaagcaag 20ftfi <
218 k   i   a   d   t   l   i   k   q   d   g   r   y   t   v   p   f   f   k   a


781 tgaaatcaaa aatatgcctg ccgctacaac taaagatgca caaactaata ctattgaacc
238 s   e   i   k   n   m   p   a   a   t   k   d   a   q   t   n   t   i   e


841 tttagatgta tgggattcat ggccagttca agatgttcgg acaggacaag ttgctaattg  5ftf >
258 p   l   d   v   w   d   s   w   p   v   q   d   v   r   t   g   q   v   a   n   8ftfi <


901 gaatggctat caacttgtca tcgcaatgat gggaattcca aaccaaaatg ataatcatat
278 w   n   g   y   q   l   v   i   a   m   m   g   i   p   n   q   n   d   n   h


 961 ctatctctta tataataagt atggtgataa tgaattaagt cattggaaga atgtaggtcc  7ftf >
 298 i   y   l   l   y   n   k   y   g   d   n   e   l   s   h   w   k   n   v   g


1021 aattttggc tataattcta ccgcggtttc acaagaatgg tcaggatcag ctgttttgaa  7ftf >
318 p   i   f   g   y   n   s   t   a   v   s   q   e   w   s   g   s   a   v   l   6ftfi <


1081 cagtgataac tctatccaat tattttatac aagggtagac acgtctgata acaataccaa
338 n   s   d   n   s   i   q   l   f   y   t   r   v   d   t   s   d   n   n   t


1141 tcatcaaaaa attgctagcg ctactcttta tttaactgat aataatggaa atgtatcact  NheI
358 n   h   q   k   i   a   s   a   t   l   y   l   t   d   n   n   g   n   v   s  AC1(i)<>


1201 cgctcaggta cgaaatgact atattgtatt tgaaggtgat ggctattact accaaactta AC2(i)<>
378 l   a   q   v   r   n   d   y   i   v   f   e   g   d   g   y   y   y   q   t


1261 tgatcaatgg aaagctacta acaaaggtgc cgataatatt gcaatgcgtg atgctcatgt
398 y   d   q   w   k   a   t   n   k   g   a   d   n   i   a   m   r   d   a   h
```

Fig 1 (3)

```
1321 aattgaagat ggtaatggtg atcggtacct tgtttttgaa gcaagtactg gtttggaaaa
 418 v  i  e  d  g  n  g  d  r  y  l  v  f  e  a  s  t  g  l  e

1381 ttatcaaggc gaggaccaaa tttataactg gttaaattat ggcggagatg acgcatttaa
 438 n  y  q  g  e  d  q  i  y  n  w  l  n  y  g  g  d  d  a  f

1441 tatcaagagc ttatttagaa ttctttccaa tgatgatatt aagagtcggg caacttgggc
 458 n  i  k  s  l  f  r  i  l  s  n  d  d  i  k  s  r  a  t  w

1501 taatgcagct atcggtatcc tcaaactaaa taaggacgaa aagaatccta aggtggcaga
 478 a  n  a  a  i  g  i  l  k  l  n  k  d  e  k  n  p  k  v  a

1561 gttatactca ccattaattt ctgcaccaat ggtaagcgat gaaattgagc gaccaaatgt
 498 e  l  y  s  p  l  i  s  a  p  m  v  s  d  e  i  e  r  p  n

1621 agttaaatta ggtaataaat attacttatt tgccgctacc cgtttaaatc gaggaagtaa
 518 v  v  k  l  g  n  k  y  y  l  f  a  a  t  r  l  n  r  g  s

1681 tgatgatgct tggatgaatg ctaattatgc cgttggtgat aatgttgcaa tggtcggata
 538 n  d  d  a  w  m  n  a  n  y  a  v  g  d  n  v  a  m  v  g

1741 tgttgctgat agtctaactg gatcttataa gccattaaat gattctggag tagtcttgac
 558 y  v  a  d  s  l  t  g  s  y  k  p  l  n  d  s  g  v  v  l

1801 tgcttctgtt cctgcaaact ggcggacagc aacttattca tattatgctg tccccgttgc
 578 t  a  s  v  p  a  n  w  r  t  a  t  y  s  y  y  a  v  p  v

1861 cggaaaagat gaccaagtat tagttacttc atatatgact aatagaaatg gagtagcggg
 598 a  g  k  d  d  q  v  l  v  t  s  y  m  t  n  r  n  g  v  a

1921 taaaggaatg gattcaactt gggcaccgag tttcttacta caaattaacc cggataacac 12ftfi <
 618 g  k  g  m  d  s  t  w  a  p  s  f  l  l  q  i  n  p  d  n
```

Fig 1 (4)

```
1981 aactactgtt ttagctaaaa tgactaatca aggggattgg atttgggatg attcaagcga
 638 t    t    t    v    l    a    k    m    t    n    q    g    d    w    i    w    d    d    s    s

2041 aaatcttgat atgattggtg atttagactc cgctgcttta cctggcgaac gtgataaacc
 658 e    n    l    d    m    i    g    d    l    d    s    a    a    l    p    g    e    r    d    k

2101 tgttgattgg gacttaattg gttatggatt aaaaccgcat gatcctgcta caccaaatga
 678 p    v    d    w    d    l    i    g    y    g    l    k    p    h    d    p    a    t    p    n

2161 tcctgaaacg ccaactacac cagaaacccc tgagacacct aatactccca aaacaccaaa
 698 d    p    e    t    p    t    t    p    e    t    p    e    t    p    n    t    p    k    t    p

2221 gactcctgaa aatcctggga cacctcaaac tcctaataca cctaatactc cggaaattcc
 718 k    t    p    e    n    p    g    t    p    g    t    p    n    t    p    n    t    p    e    i

2281 tttaactcca gaaacgccta agcaacctga aacccaaact aataatcgtt tgccacaaac
 738 p    l    t    p    e    t    p    k    q    p    e    t    q    t    n    n    r    l    p    q

2341 tggaaataat gccaataaag ccatgattgg cctaggtatg ggaacattgc ttagtatgtt
 758 t    g    n    n    a    n    k    a    m    i    g    l    g    m    g    t    l    l    s    m

2401 tggtcttgca gaaattaaca aacgtcgatt taactaaata ctttaaaata aaaccgctaa
 778 f    g    l    a    e    i    n    k    r    r    f    n    -

2461 gccttaaatt cagcttaacg gtttttttatt ttaaaagttt ttattgtaaa aaagcgaatt

2521 atcattaata ctaatgcaat tgttgtaaga ccttacgaca gtagtaacaa tgaatttgcc

2581 catctttgtc gg                                                    NheI
```

Fig 2

Distance
10%

71

100

99

100

100

85

100

100

100

100

77

71

Zymomonas mobilis SacB

Zymomonas mobilis LevU

Zymomonas mobilis SucE2

Erwinia amylovora Lsc

Acetobacter diazotrophicus LsdA

Cynara scolymus Ss-1ft

Hordeum vulgare Sf-6ft

Allium cepa F-6gft

Bacillus stearothermophilus SurB

Bacillus subtilis SacB

Bacillus amyloliquefaciens SacB

Lactobacillus reuteri FTFB

Streptococcus salivarius Ftf

Lactobacillus reuteri FTFA
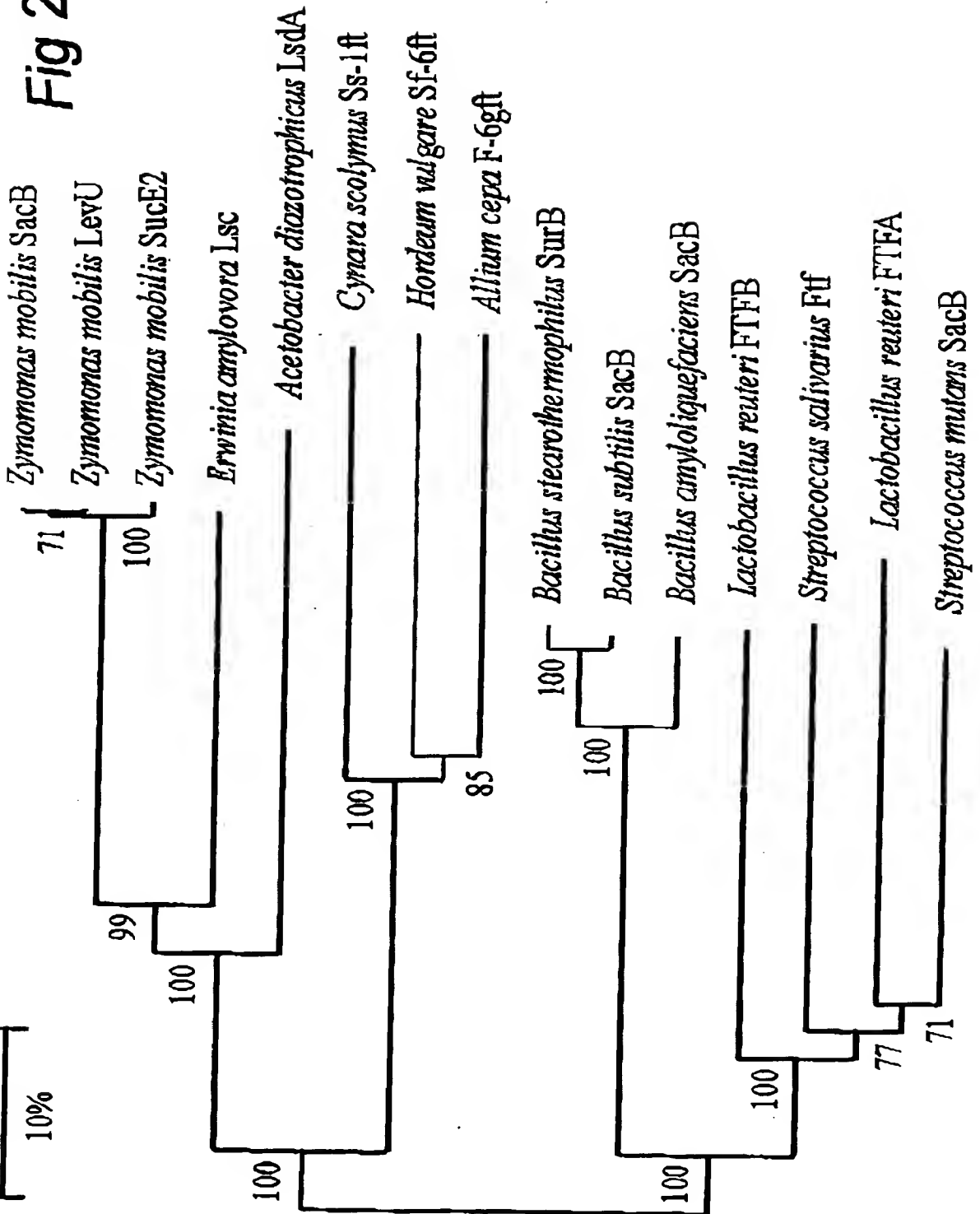
Streptococcus mutans SacB

Fig 3

The N-terminal sequence of FTFB (levansucrase):
(A) Q V E S N N Y N G V A E V N T E R Q A N G Q I (G) (V) (D).

Internal peptide sequences of FTFB (levansucrase):

- (M) (A) H L D V W D S W P V Q D P (V),
- N A G S I F G T (K),
- V (E) (E) V Y S P K V S T L M A S D E V E.

Fig 4

`LGGKLFTVGGGGGG`

5ftf

B. amyloliquefaciens SacB	80	GLDVWDSWPLQNAD	93
B. subtilis SacB	82	GLDVWDSWPLQNAD	95
S. mutans SacB	243	DLDVWDSWPVQDAK	256
S. salivarius Ftf	282	EIDVWDSWPVQDAK	295
		:.********.*.:*.	

6ftfi

B. amyloliquefaciens SacB	156	QTQEWSGSATFTSDGK	171
B. subtilis SacB	158	QTQEWSGSATFTSDGK	173
S. mutans SacB	312	LTQEWSGSATVNEDGS	327
S. salivarius Ftf	351	DDQQWSGSATVNSDGS	366
		*.:*******...**.	

12ftfi

B. amyloliquefaciens SacB	440	KATFGPSFLMN	450
B. subtilis SacB	440	QSTFAPSFLIN	450
S. mutans SacB	609	NSTWAPSFLIQ	619
S. salivarius Ftf	655	KSTWAPSFLIK	665
		:.*:.*****::	

Fig 5